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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. |
|-----------------|-------------|----------------------|---------------------|
|-----------------|-------------|----------------------|---------------------|

09/479,877 01/10/00 WOLF

M

EXAMINER

HM22/0212

ELIZABETH ARWINE PATENT ATTORNEY
U S ARMY MEDICAL RESEARCH & MATERIEL COM
504 SCOTT STREET
FORT DETRICK MD 21702-5021

PORTNER, V

ART UNIT

PAPER NUMBER

1645

DATE MAILED:

02/12/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

USAMRMC
STAFF JUDGE ADVOCATE
FORT DETRICK, MD
2001 FEB 15 PM 3:13



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Washington, D.C. 20231

| SERIAL NUMBER | FILING DATE | FIRST NAMED APPLICANT | ATTORNEY DOCKET NO. |
|---------------|-------------|-----------------------|---------------------|
| 09/479,877 | 1/10/2000 | Wolf et al | |

| EXAMINER | |
|----------|--------------|
| Portner | |
| ART UNIT | PAPER NUMBER |
| 1645 | 5 |

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

2. Applicant is given ONE MONTH, or THIRTY DAYS, whichever is longer, from the mailing date of this letter within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). In no case may an applicant extend the period for reply beyond the SIX MONTH statutory period. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ginny Portner whose telephone number is (703)308-7543. The examiner can normally be reached on Monday through Friday from 7:30 AM to 5:00 PM except for the first Friday of each two week period.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith, can be reached on (703) 308-3909. The fax phone number for this group is (703) 308-4242.

The Group and/or Art Unit location of your application in the PTO will be Group Art Unit 1645. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to this Art Unit.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

LZ8

LYNETTE R. F. SMITH
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

NOTICE TO COMPLY WITH: REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: additional sequences found

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wolf, Marcia K
Cassels, Fred J
Boedeker, Edgar C
- (ii) TITLE OF INVENTION: Transformed Bacteria Producing GS6
Antigens as Vaccines
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hendricks and Assoc
 - (B) STREET: P.O. Box 2509
 - (C) CITY: Fairfax
 - (D) STATE: VA
 - (E) COUNTRY: US
 - (F) ZIP: 22031
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/479,877
 - (B) FILING DATE: 10-JAN-2000
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hendricks, Glenna M
 - (B) REGISTRATION NUMBER: 32,535
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703/425-8405
 - (B) TELEFAX: 703/425-8406

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|------------|------------|-------------|-------------|------------|------------|------|
| AAGCTTGTA | CCAGTTGATA | AAAATATATC | ACGCTGGGAA | TGACGTGATG | TATATACGGA | 60 |
| GCAGCTATGT | CGGAACAGAT | ATTTTCCTAT | CGGTATGCGT | TGTGAGTAAG | CGTAAAGCCA | 120 |
| ATGCTGTCTG | TAACCTCTGA | TCCTTGCAGA | CTAAATTAGA | GCTCCTTCTA | AATTAGACGG | 180 |
| ATGGATAAAC | CTACAGACTG | GCGCTCTGGG | TCTCGCCGGA | TATTTTCTAA | TGAATTTAAG | 240 |
| CTTCATATGG | TTGAACTGGC | TTCGAAACCA | AATGCCAATG | TCGCACAACT | GGCTCGGGAA | 300 |
| CATGGCGTTG | ATAACAACCT | GATTTTTTAAA | TAGCTACGCC | TCTGGCAAAG | AGAAGGACGT | 360 |
| ATTTCTCGTA | GAATGCCTCC | AACTATTGTA | GGCCCTACAG | TACCACTGAG | GTAGCCTGAA | 420 |
| TTTAAAGCCG | AAGCGGTCAG | AACTGTTCTT | GGTGTGAACG | TAGCACTCAC | CAATAAAAGC | 480 |
| ATCAATACGG | TGCTCTGTTG | ACACATTACG | AATGTTATGT | ATACAATAAA | AATGATTATA | 540 |
| GCAATATTAA | TGGTGTTATA | TGAAGAAAAC | AATTGGTTTA | ATTCTAATTC | TTGCTTCATT | 600 |
| CGGCAGCCAT | GCCAGAACAG | AAATAGCGAC | TAAAAACTTC | CCAGTATCAA | CGACTATTTT | 660 |
| AAAAAGTTTT | TTTGCACCTG | AACCACGAAT | ACAGCCTTCT | TTTGGTGAAA | ATGTTGGAAA | 720 |
| GGAAGGAGCT | TTATTATTTA | GTGTGAACTT | AACTGTTCCCT | GAAAATGTAT | CCCAGGTAAC | 780 |
| GGTCTACCCT | GTTTATGATG | AAGATTATGG | GTTAGGACGA | CTAGTAAATA | CCGCTGATGC | 840 |
| TTCCCAATCA | ATAATCTACC | AGATTGTTGA | TGAGAAAGGG | AAAAAAATGT | TAAAAGATCA | 900 |
| TGGTGCAGAG | GTTACACCTA | ATCAACAAAT | AACTTTTAAA | GCGCTGAATT | ATACTAGCGG | 960 |
| GGAAAAAAA | ATATCTCCTG | GAATATATAA | CGATCAGGTT | ATGGTTGGTT | ACTATGTAAA | 1020 |
| CTAAATACTG | GAAGTATGAT | TATGTTGAAA | AAAATTATTT | CGGCTATTGC | ATTAATTGCA | 1080 |
| GGAAGTTCCG | GAGTGGTAAA | TGCAGGAAAC | TGGCAATATA | AATCTCTGGA | TGTAAATGTA | 1140 |
| AATATTGAGC | AAAATTTTAT | TCCAGATATT | GATTCCGCTG | TTCGTATAAT | ACCTGTTAAT | 1200 |
| TACGATTCGG | ACCCGAAACT | GGATTCACAG | TTATATACGG | TTGAGATGAC | GATCCCTGCA | 1260 |
| GGTGTAAGCG | CAGTTAAAAT | CGCACCAACA | GATAGTCTGA | CATCTTCTGG | ACAGCAGATC | 1320 |
| GGAAAGCTGG | TTAATGTAAA | CAATCCAGAT | CAAAATATGA | ATTATTATAT | CAGAAAGGAT | 1380 |
| TCTGGCGCTG | GTAACTTTAT | GGCAGGACAA | AAAGGATCCT | TTCCTGTCAA | AGAGAATACG | 1440 |
| TCATACACAT | TCTCAGCAAT | TTATACTGGT | GGCGAATACC | CTAATAGCGG | ATATTCGTCT | 1500 |

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|------|
| GGTACTTATG | CAGGAAATTT | GACTGTATCA | TTTTACAGCA | ATTAAAAAAA | GGCCGCATTA | 1560 |
| TTGCGGCCAT | TGACGATACT | GCTAGGCAAA | AATATGAAAT | CAAAGTTAAT | TATACTATTG | 1620 |
| ACGTTAGTGC | CATTTTCATC | TTTTTCAACA | GGAAATAATT | TTGAAATAAA | TAAGACACGA | 1680 |
| GTAATTTACT | CTGACAGCAC | ACCATCAGTT | CAAATATCAA | ATAATAAAGC | ATATCCTTTA | 1740 |
| ATTATTCAAA | GCAATGTATG | GGATGAAAGC | AATAATAAAA | ATCATGACTT | TATAGCAACA | 1800 |
| CCACCGATTT | TTAAAATGGA | AAGTGAAAGT | CGGAATATAA | TAAAAATAAT | TAAAACAAC | 1860 |
| ATTAATTTGC | CGGACTCTCA | GGAAAGTATG | AGATGGTTAT | GTATTGAATC | AATGCCACCA | 1920 |
| ATAGAAAAAA | GTACTAAAAT | AAACAGAAAA | GAAGGAAGGA | CAGACAGTAT | TAATATCAGC | 1980 |
| ATTCGGGGGT | GCATTAAACT | GATATATCGA | CCTGCCAGTG | TTCCGTCTCC | TGTTTTTAAT | 2040 |
| AATATAGTAG | AAAAATTAAA | ATGGCATAAA | AATGGAAAGT | ATCTTGATT | AAAAATAAT | 2100 |
| ACACCCTATT | ACATTAGCTT | TTCTGAGGTT | TTTTTTGATT | CAGATAAAGT | AAACAATGCA | 2160 |
| AAAGATATTT | TATATGTAAA | ACCATACTCA | GAGAAGAAAA | TAGATATCAG | CAACAGAATA | 2220 |
| ATAAAAAAAA | TCAAATGGGC | TATGATTGAT | GATGCTGGCG | CAAAAACAAA | ACTTTATGAA | 2280 |
| TCAATTTTAT | AAAAATCTC | ATTACAGTAT | ACAAAAACAT | CAGATTACAG | GCTTGCTTTT | 2340 |
| TTTGCTATTT | ATATATCCTT | TCTCAACCTC | ATATGGAAAT | GAACAATTTA | GTTTTGACTC | 2400 |
| ACGATTCCTA | CCATCAGGTT | ATAATTACTC | TTTAAATAGT | AACTTACCTC | CTGAAGGTGA | 2460 |
| GTATCTGGTT | GATATTTATA | TTAACAAAAT | AAAAAAGGAG | TCCGCGATTA | TTCTTTTTTA | 2520 |
| TATAAAAGGA | AATAAACTTG | TACCATGTTT | ATCAAAAGAA | AAAATTTTCAT | CTTTGGGTAT | 2580 |
| CAACATTAAT | AATAACGACA | ACACAGAGTG | TGTAGAAACA | AGTAAGGCAG | GTATTAGTAA | 2640 |
| TATCAGCTTT | GAGTTTAGCT | CTCTTCGTTT | GTTTATTGCT | GTACCGAAAA | ATCTTCTGTC | 2700 |
| TGAGATTGAT | AAAATATCAT | CAAAGGATAT | AGATAACGGG | ATTCATGCTT | TATTTTTTAA | 2760 |
| TTATCAAGTA | AATACAAGGC | TAGCCAATAA | TAAAAATCGT | TATGATTACA | TTTCTGTTTC | 2820 |
| ACCAAATATA | AATTATTTTT | CATGGCGGTT | GCGTAATCTT | TTTGAATTTA | ACCAAAACAA | 2880 |
| CGATGAAAAA | ACATGGGAAA | GAAACTACAC | TTATCTAGAA | AAAAGTTTTT | ATGATAAAAA | 2940 |
| GCTAAACTTA | GTCGTTGGTG | AAAGTTATAC | GAATTCAAAT | GTTTATAATA | ACTACTCTTT | 3000 |
| TACTGGTATT | TCAGTTTCTA | CAGATACAGA | TATGTATACG | CCAAGTGAAA | TCGATTATAC | 3060 |
| ACCAGAAATT | CATGGAGTGG | CTGATTCAGA | CTCTCAGATT | ATTGTCAGGC | AAGGCAACAC | 3120 |

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|------|
| CATTATCATT | AATGAAAGTG | TTCCAGCCGG | ACCGTTCTCA | TTTCCAATAA | CCAATCTCAT | 3180 |
| GTATACTGGG | GGGCAACTTA | ATGTGGAGAT | AACAGATATT | TATGGAAATA | AAAAACAATA | 3240 |
| TACTGTCAAT | AATTCCTCTC | TTCCTGTTAT | GAGAAAAGCG | GGACTAATGG | TATATAATTT | 3300 |
| TATATCTGGG | AAATTAACAA | AAAAAAATAG | TGAGGATGGT | GATTTTTTTTA | CTCAAGGTGA | 3360 |
| TATTAACTAC | GGTACTCACT | ATAACAGCAC | ACTATTCGGT | GGATATCAGT | TTAGTAAAAA | 3420 |
| TTATTTTAAC | TTATCTACTG | GTATAGGCAC | TGATCTGGGA | TTTCTGGAG | CATGGCTACT | 3480 |
| ACACGTTAGC | AGAAGTAATT | TTAAGAATAA | AAATGGATAT | AATATTAATC | TACAACAAAA | 3540 |
| CACTCAGTTA | AGACCATTCA | ATGCCGGGGT | TAATTTTCGAT | TACGCATACA | GAAAAAAAAG | 3600 |
| GTATGTGGAA | CTTTCCGACA | TTGGCTGGCA | TGGTAATTTA | TATAATCAAC | TTAAAAATAG | 3660 |
| TTTTTCTTTA | TCCTTGTCAA | AATCATTGAA | TAAATACGGA | AATTTCTCAC | TTGATTATAA | 3720 |
| CAAAATGAAA | TACTGGGATA | ATGCGTATGA | TAGTAACTCA | ATGTCGATTC | GTTATTTTTT | 3780 |
| TAAATTCATG | CGAGCAATGA | TTACAACAAA | TTGTTCTTTA | AATAAATATC | AATCTTATGA | 3840 |
| AAAAAAAGAT | AAAAGATTTA | GTATTAATAT | ATCATTGCCT | TTAACCAAAG | ATTACGGGCA | 3900 |
| CATATCTTCA | AACTATTCAT | TTTCCAATGC | AAATACAGGA | ACGGCAACCA | GTTCTGTAGG | 3960 |
| CTTAAACGGT | AGTTTTTTTA | ATGACGCAAG | ATTAAACTGG | AACATTCAGC | AGAACAGAAC | 4020 |
| GACCCGTAAC | AATGGATATA | CTGATAATAC | CAGTTACATA | GCAACCAGCT | ATGCCTCTCC | 4080 |
| CTATGGCGTT | TTTACTGGTT | CATATTCAGG | ATCGAACAAG | TATTCAAGCC | AGTTTTATTC | 4140 |
| TGCATCGGGA | GGTATTGTTT | TGCATAGCGA | TGGCGTAGCT | TTTACTCAAA | AAGCCGGAGA | 4200 |
| TACCTCTGCT | CTTGTCCGTA | TTGATAATAT | TTCTGATATA | AAAATTGGTA | ACACTCCTGG | 4260 |
| TGTTTATACT | GGGTATAATG | GTTTTGCTTT | AATTCCTCAT | CTTCAGCCGT | TCAAAAAAAA | 4320 |
| CACCATTTTA | ATTAATGATA | AAGGAATTCC | AGACGGTATT | ACTCTTGCTA | ATATAAAAAA | 4380 |
| ACAAGTTATC | CCATCACGAG | GAGCTATTGT | TAAAGTAAAA | TTTGATGCTA | AAAAAGGCAA | 4440 |
| TGACATTTTG | TTTAAGCTTA | CAACTAAAGA | TGGAAAAACG | CCCCATTAG | GAGCTATAGC | 4500 |
| CCATGAAAAA | AATGGAAAAC | AGATTAATAC | GGGTATCGTT | GACGATGATG | GTATGCTTTA | 4560 |
| TATGTCTGGA | TTATCAGGGA | CAGGGATTAT | TAATGTAACA | TGGAATGGAA | AAGTCTGTTC | 4620 |
| ATTCCTTTT | TCAGAAAAAG | ATATATCTAG | CAAACAATTA | TCTGTTGTAA | ATAACAATG | 4680 |
| TTAGGTAGTG | CATCCAATTA | GTAGAACATG | TGTTTTTCGA | TAAACGCTCC | GATCTCTTTT | 4740 |

TCGTGGATCT CAACTGAGCG TGAGAAGCAG ATTGTTTTAC GAGCCAACCG CTTAATGCGG 4800
GTGCGTAGCG TCAGATTATT ACGCTCAATG CGTTGGGTGA ATATTTTGCC GGTCAGATGC 4860
TTATTCTTCG GTACC 4875

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCCGCATTA TTGCGGCC

18

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCGCATTA TTGATTGCGG CC

22

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 527 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTGACACATT | ACGAATGTTA | TGTATACAAT | AAAAATGATT | ATAGCAATAT | TAATGGTGTT | 60 |
| ATATGAAGAA | AACAATTGGT | TTAATTCTAA | TTCTTGCTTC | ATTCGGCAGC | CATGCCAGAA | 120 |
| CAGAAATAGC | GAATAAAAAC | TTCCCAGTAT | CAACGACTAT | TTCAAAAAGT | TTTTTTGCAC | 180 |
| CTGAACCACG | AATACAGCCT | TCTTTTGGTG | AAAATGTTGG | AAAGGAAGGA | GCTTTATTAT | 240 |
| TTAGTGTGAA | CTTAACTGTT | CCTGAAAATG | TATCCCAGGT | AACGGTCTAC | CCTGTTTATG | 300 |
| ATGAAGATTA | TGGGTTAGGA | CGACTAGTAA | ATACCGCTGA | TGCTTCCCAA | TCAATAATCT | 360 |
| ACCAGATTGT | TGATGAGAAA | GGGAAAAAAA | TGTTAAAAGA | TCATGGTGCA | GAGGTTACAC | 420 |
| CTAATCAACA | AATAACTTTT | AAAGCGCTGA | ATTATACTAG | CGGGGAAAAA | AAAATATCTC | 480 |
| CTGGAATATA | TAACGATCAG | GTTATGGTTG | GTTACTATGT | AAACTAA | | 527 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Thr | Ile | Gly | Leu | Ile | Leu | Ile | Leu | Ala | Ser | Phe | Gly | Ser |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Ala | Arg | Thr | Glu | Ile | Ala | Thr | Lys | Asn | Phe | Pro | Val | Ser | Thr | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Lys | Ser | Phe | Phe | Ala | Pro | Glu | Pro | Arg | Ile | Gln | Pro | Ser | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Glu | Asn | Val | Gly | Lys | Glu | Gly | Ala | Leu | Leu | Phe | Ser | Val | Asn | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |

Thr Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp
 65 70 75 80

Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln
 85 90 95

Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys
 100 105 110

Asp His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala
 115 120 125

Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn
 130 135 140

Asp Gln Val Met Val Gly Tyr Tyr Val Asn
 145 150

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ile Ile Ser Ala Ile Ala Leu Ile Ala Gly Thr Ser
 1 5 10 15

Gly Val Val Asn Ala Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn
 20 25 30

Val Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg
 35 40 45

Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu
 50 55 60

Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile
 65 70 75 80
 Ala Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu
 85 90 95
 Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys
 100 105 110
 Asp Ser Gly Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro
 115 120 125
 Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly
 130 135 140
 Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu
 145 150 155 160
 Thr Val Ser Phe Tyr Ser Asn
 165

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 212 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Asn Phe Glu Ile Asn Lys Thr Arg Val Ile Tyr Ser Asp Ser Thr
 1 5 10 15
 Pro Ser Val Gln Ile Ser Asn Asn Lys Ala Tyr Pro Leu Ile Ile Gln
 20 25 30
 Ser Asn Val Trp Asp Glu Ser Asn Asn Lys Asn His Asp Phe Ile Ala
 35 40 45

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Pro | Pro | Ile | Phe | Lys | Met | Glu | Ser | Glu | Ser | Arg | Asn | Ile | Ile | Lys | |
| 50 | | | | | | 55 | | | | | 60 | | | | | |
| Ile | Ile | Lys | Thr | Thr | Ile | Asn | Leu | Pro | Asp | Ser | Gln | Glu | Ser | Met | Arg | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Trp | Leu | Cys | Ile | Glu | Ser | Met | Pro | Pro | Ile | Glu | Lys | Ser | Thr | Lys | Ile | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Asn | Arg | Lys | Glu | Gly | Arg | Thr | Asp | Ser | Ile | Asn | Ile | Ser | Ile | Arg | Gly | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Cys | Ile | Lys | Leu | Ile | Tyr | Arg | Pro | Ala | Ser | Val | Pro | Ser | Pro | Val | Phe | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Asn | Asn | Ile | Val | Glu | Lys | Leu | Lys | Trp | His | Lys | Asn | Gly | Lys | Tyr | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Val | Leu | Lys | Asn | Asn | Thr | Pro | Tyr | Tyr | Ile | Ser | Phe | Ser | Glu | Val | Phe | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Phe | Asp | Ser | Asp | Lys | Val | Asn | Asn | Ala | Lys | Asp | Ile | Leu | Tyr | Val | Lys | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Pro | Tyr | Ser | Glu | Lys | Lys | Ile | Asp | Ile | Ser | Asn | Arg | Ile | Ile | Lys | Lys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Ile | Lys | Trp | Ala | Met | Ile | Asp | Asp | Ala | Gly | Ala | Lys | Thr | Lys | Leu | Tyr | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Glu | Ser | Ile | Leu | | | | | | | | | | | | | |
| | | | 210 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asn | Gln | Phe | Tyr | Lys | Lys | Ser | His | Tyr | Ser | Ile | Gln | Lys | His | Gln | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ile | Thr | Gly | Leu | Leu | Phe | Leu | Leu | Phe | Ile | Tyr | Pro | Phe | Ser | Thr | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Gly | Asn | Glu | Gln | Phe | Ser | Phe | Asp | Ser | Arg | Phe | Leu | Pro | Ser | Gly | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Tyr | Asn | Tyr | Ser | Leu | Asn | Ser | Asn | Leu | Pro | Pro | Glu | Gly | Glu | Tyr | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Val | Asp | Ile | Tyr | Ile | Asn | Lys | Ile | Lys | Lys | Glu | Ser | Ala | Ile | Ile | Pro | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Phe | Tyr | Ile | Lys | Gly | Asn | Lys | Leu | Val | Pro | Cys | Leu | Ser | Lys | Glu | Lys | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ile | Ser | Ser | Leu | Gly | Ile | Asn | Ile | Asn | Asn | Asn | Asp | Asn | Thr | Glu | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Val | Glu | Thr | Ser | Lys | Ala | Gly | Ile | Ser | Asn | Ile | Ser | Phe | Glu | Phe | Ser | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Ser | Leu | Arg | Leu | Phe | Ile | Ala | Val | Pro | Lys | Asn | Leu | Leu | Ser | Glu | Ile | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Asp | Lys | Ile | Ser | Ser | Lys | Asp | Ile | Asp | Asn | Gly | Ile | His | Ala | Leu | Phe | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Phe | Asn | Tyr | Gln | Val | Asn | Thr | Arg | Leu | Ala | Asn | Asn | Lys | Asn | Arg | Tyr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Asp | Tyr | Ile | Ser | Val | Ser | Pro | Asn | Ile | Asn | Tyr | Phe | Ser | Trp | Arg | Leu | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Arg | Asn | Leu | Phe | Glu | Phe | Asn | Gln | Asn | Asn | Asp | Glu | Lys | Thr | Trp | Glu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Asn | Tyr | Thr | Tyr | Leu | Glu | Lys | Ser | Phe | Tyr | Asp | Lys | Lys | Leu | Asn | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Leu | Val | Val | Gly | Glu | Ser | Tyr | Thr | Asn | Ser | Asn | Val | Tyr | Asn | Asn | Tyr | |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 | |
| Ser | Phe | Thr | Gly | Ile | Ser | Val | Ser | Thr | Asp | Thr | Asp | Met | Tyr | Thr | Pro | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ser | Glu | Ile | Asp | Tyr | Thr | Pro | Glu | Ile | His | Gly | Val | Ala | Asp | Ser | Asp | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ser | Gln | Ile | Ile | Val | Arg | Gln | Gly | Asn | Thr | Ile | Ile | Ile | Asn | Glu | Ser | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Val | Pro | Ala | Gly | Pro | Phe | Ser | Phe | Pro | Ile | Thr | Asn | Leu | Met | Tyr | Thr | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Gly | Gly | Gln | Leu | Asn | Val | Glu | Ile | Thr | Asp | Ile | Tyr | Gly | Asn | Lys | Lys | |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 | |
| Gln | Tyr | Thr | Val | Asn | Asn | Ser | Ser | Leu | Pro | Val | Met | Arg | Lys | Ala | Gly | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Leu | Met | Val | Tyr | Asn | Phe | Ile | Ser | Gly | Lys | Leu | Thr | Lys | Lys | Asn | Ser | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Glu | Asp | Gly | Asp | Phe | Phe | Thr | Gln | Gly | Asp | Ile | Asn | Tyr | Gly | Thr | His | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Tyr | Asn | Ser | Thr | Leu | Phe | Gly | Gly | Tyr | Gln | Phe | Ser | Lys | Asn | Tyr | Phe | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Asn | Leu | Ser | Thr | Gly | Ile | Gly | Thr | Asp | Leu | Gly | Phe | Ser | Gly | Ala | Trp | |
| | 385 | | | | 390 | | | | | 395 | | | | | 400 | |
| Leu | Leu | His | Val | Ser | Arg | Ser | Asn | Phe | Lys | Asn | Lys | Asn | Gly | Tyr | Asn | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Ile | Asn | Leu | Gln | Gln | Asn | Thr | Gln | Leu | Arg | Pro | Phe | Asn | Ala | Gly | Val | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |

Asn Phe Asp Tyr Ala Tyr Arg Lys Lys Arg Tyr Val Glu Leu Ser Asp
 435 440 445

Ile Gly Trp His Gly Asn Leu Tyr Asn Gln Leu Lys Asn Ser Phe Ser
 450 455 460

Leu Ser Leu Ser Lys Ser Leu Asn Lys Tyr Gly Asn Phe Ser Leu Asp
 465 470 475 480

Tyr Asn Lys Met Lys Tyr Trp Asp Asn Ala Tyr Asp Ser Asn Ser Met
 485 490 495

Ser Ile Arg Tyr Phe Phe Lys Phe Met Arg Ala Met Ile Thr Thr Asn
 500 505 510

Cys Ser Leu Asn Lys Tyr Gln Ser Tyr Glu Lys Lys Asp Lys Arg Phe
 515 520 525

Ser Ile Asn Ile Ser Leu Pro Leu Thr Lys Asp Tyr Gly His Ile Ser
 530 535 540

Ser Asn Tyr Ser Phe Ser Asn Ala Asn Thr Gly Thr Ala Thr Ser Ser
 545 550 555 560

Val Gly Leu Asn Gly Ser Phe Phe Asn Asp Ala Arg Leu Asn Trp Asn
 565 570 575

Ile Gln Gln Asn Arg Thr Thr Arg Asn Asn Gly Tyr Thr Asp Asn Thr
 580 585 590

Ser Tyr Ile Ala Thr Ser Tyr Ala Ser Pro Tyr Gly Val Phe Thr Gly
 595 600 605

Ser Tyr Ser Gly Ser Asn Lys Tyr Ser Ser Gln Phe Tyr Ser Ala Ser
 610 615 620

Gly Gly Ile Val Leu His Ser Asp Gly Val Ala Phe Thr Gln Lys Ala
 625 630 635 640

Gly Asp Thr Ser Ala Leu Val Arg Ile Asp Asn Ile Ser Asp Ile Lys
 645 650 655

Ile Gly Asn Thr Pro Gly Val Tyr Thr Gly Tyr Asn Gly Phe Ala Leu
 660 665 670

Ile Pro His Leu Gln Pro Phe Lys Lys Asn Thr Ile Leu Ile Asn Asp
 675 680 685

Lys Gly Ile Pro Asp Gly Ile Thr Leu Ala Asn Ile Lys Lys Gln Val
 690 695 700

Ile Pro Ser Arg Gly Ala Ile Val Lys Val Lys Phe Asp Ala Lys Lys
 705 710 715 720

Gly Asn Asp Ile Leu Phe Lys Leu Thr Thr Lys Asp Gly Lys Thr Pro
 725 730 735

Pro Leu Gly Ala Ile Ala His Glu Lys Asn Gly Lys Gln Ile Asn Thr
 740 745 750

Gly Ile Val Asp Asp Asp Gly Met Leu Tyr Met Ser Gly Leu Ser Gly
 755 760 765

Thr Gly Ile Ile Asn Val Thr Trp Asn Gly Lys Val Cys Ser Phe Pro
 770 775 780

Phe Ser Glu Lys Asp Ile Ser Ser Lys Gln Leu Ser Val Val Asn Lys
 785 790 795 800

Gln Cys

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser
 1 5 10 15

Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe Gly Glu
 20 25 30

Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu Thr Val
 35 40 45

Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp
 50 55 60

Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln Ser Ile
 65 70 75 80

Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys Asp His
 85 90 95

Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn
 100 105 110

Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn Asp Gln
 115 120 125

Val Met Val Gly Tyr Tyr Val Asn
 130 135

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln
 1 5 10 15

Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn
20 25 30

Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met
35 40 45

Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser
50 55 60

Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn
65 70 75 80

Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly
85 90 95

Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr
100 105 110

Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser
115 120 125

Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr
130 135 140

Ser Asn
145